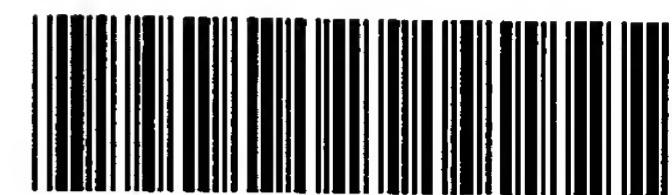


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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/028,247

DATE: 04/01/2002
TIME: 15:24:52

Input Set : A:\-335-2.app
Output Set: N:\CRF3\04012002\J028247.raw

3 <110> APPLICANT: Goldman, Stanley
 4 Lathrop, Stephanie J.
 5 Longchamp, Pascal F.
 6 Whalen, Robert G.
 7 Maxygen, Inc.
 9 <120> TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
 10 Systems for Medicinal and Industrial Applications
 12 <130> FILE REFERENCE: 18097A-033520US
 14 <140> CURRENT APPLICATION NUMBER: US 10/028,247
 15 <141> CURRENT FILING DATE: 2001-12-19
 17 <150> PRIOR APPLICATION NUMBER: US 60/214,161
 18 <151> PRIOR FILING DATE: 2000-06-26
 20 <150> PRIOR APPLICATION NUMBER: US 09/892,208
 21 <151> PRIOR FILING DATE: 2001-06-26
 23 <160> NUMBER OF SEQ ID NOS: 6
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 258
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Bacillus subtilis
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)...(258)
 35 <223> OTHER INFORMATION: CotC27 including HA11 epitope region
 37 <400> SEQUENCE: 1
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 39 Met Gly Tyr Tyr Lys Lys Tyr Lys Glu Glu Tyr Tyr Thr Val Lys Lys
 40 1 5 10 15
 42 acg tat tat aag aag tat tac gaa tat gat aaa tct aga ggt acc tgc 96
 43 Thr Tyr Tyr Lys Lys Tyr Tyr Glu Tyr Asp Lys Ser Arg Gly Thr Cys
 44 20 25 30
 46 tat cct tat gat gtt cct gat tat gct tct tta gga tcc ctg cag aaa 144
 47 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys
 48 35 40 45
 50 gat tat gac tgt gat tac gac aaa aaa tat gat gac tat gat aaa aaa 192
 51 Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys
 52 50 55 60
 54 tat tat gat cac gat aaa aaa gac tat gat tat gtt gta gag tat aaa 240
 55 Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys
 56 65 70 75 80
 58 aag cat aaa aaa cac tac 258
 59 Lys His Lys Lys His Tyr
 60 85

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63 <210> SEQ ID NO: 2
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 66 <213> ORGANISM: Bacillus subtilis
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 71 <400> SEQUENCE: 2
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 73 1 5 10 15
 74 Thr Tyr Tyr Lys Lys Tyr Tyr Glu Tyr Asp Lys Ser Arg Gly Thr Cys
 75 20 25 30
 76 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys
 77 35 40 45
 78 Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys
 79 50 55 60
 80 Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys
 81 65 70 75 80
 82 Lys His Lys Lys His Tyr
 83 85
 86 <210> SEQ ID NO: 3
 87 <211> LENGTH: 639
 88 <212> TYPE: DNA
 89 <213> ORGANISM: Bacillus circulans
 91 <220> FEATURE:
 92 <221> NAME/KEY: CDS
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 94 <223> OTHER INFORMATION: lipase 396
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 98 Met Lys Phe Ile Lys Arg Arg Ile Ile Ala Leu Val Thr Ile Leu Val
 99 1 5 10 15
 101 ctg tca gtc aca tcg ctg ttt gcg atg cag ccg tca gca aaa gcc gct 96
 102 Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala
 103 20 25 30
 105 gaa cac aat cca gtt gtt atg gtt cac ggt atc gga gga gct tca tac 144
 106 Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr
 107 35 40 45
 109 aat ttt gcg gga att aag agc tat ctc gta tct cag ggc tgg tca cgg 192
 110 Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg
 111 50 55 60
 113 ggc aag ctg tat gcg gtt gat ttt tgg gac aag aca ggg acg aat tat 240
 114 Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr
 115 65 70 75 80
 117 aac aat ggc ccg gta tta tca cga ttt gtg caa aag gtt tta gac gaa 288
 118 Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu
 119 85 90 95
 121 acg ggt gcg aaa aaa gtg gat att gtc gct cac agc atg ggt ggc gcg 336
 122 Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala
 123 100 105 110

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125	aac aca ctt tac tac ata aaa aat ctg gac ggc gga aat aaa att gaa	384
126	Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu	
127	115 120 125	
129	aac gtc gta acg ctt ggc ggc gcg aac cgt ttg acg aca agc aag gcg	432
130	Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala	
131	130 135 140	
133	ctt ccg gga aca gat cca aat caa aag att tta tac aca tcc att tac	480
134	Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr	
135	145 150 155 160	
137	agc agt gcc gat atg att gtc atg aat tac tta tca aaa tta gac ggt	528
138	Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly	
139	165 170 175	
141	gct aaa aac gtt caa att cat ggc gtt ggg cac att ggt tta ttg atg	576
142	Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met	
143	180 185 190	
145	aac agc caa gtc aac agc ctg att aaa gaa gga ctg aac ggc ggg ggc	624
146	Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly	
147	195 200 205	
149	ctc aat aca aat taa	639
150	Leu Asn Thr Asn	
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155	<211> LENGTH: 212	
156	<212> TYPE: PRT	
157	<213> ORGANISM: Bacillus circulans	
159	<220> FEATURE:	
160	<223> OTHER INFORMATION: lipase 396	
162	<400> SEQUENCE: 4	
163	Met Lys Phe Ile Lys Arg Arg Ile Ile Ala Leu Val Thr Ile Leu Val	
164	1 5 10 15	
165	Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala	
166	20 25 30	
167	Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr	
168	35 40 45	
169	Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg	
170	50 55 60	
171	Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr	
172	65 70 75 80	
173	Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu	
174	85 90 95	
175	Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala	
176	100 105 110	
177	Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu	
178	115 120 125	
179	Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala	
180	130 135 140	
181	Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr	
182	145 150 155 160	
183	Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly	

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184 165 170 175
185 Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met
186 180 185 190
187 Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly
188 195 200 205
189 Leu Asn Thr Asn
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193 <210> SEQ ID NO: 5
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195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
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199 <223> OTHER INFORMATION: Description of Artificial Sequence:primer for
200 fusion protein
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207 <211> LENGTH: 32
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence:primer for
213 terminator
215 <400> SEQUENCE: 6
216 atatctgcag ttaatttgta ttgaggcccc cg 32

VERIFICATION SUMMARY

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